

AMENDMENTS TO THE CLAIMS

Applicant has submitted a new complete claim set showing marked up claims with insertions indicated by underlining and deletions indicated by strikeouts and/or double bracketing. This listing of claims will replace all prior versions and listings of claims in the application:

1.-148. (Canceled)

149. (Currently amended) A method comprising:

preparing a randomly primed PCR-derived reduced complexity genome (RCG) using at least one polymerase chain reaction (PCR) primer, wherein the RCG contains less than 20% of genomic material present in a whole genome,

contacting single nucleotide polymorphisms – allele specific oligonucleotides (SNP-ASOs) immobilized on a surface with the RCG under hybridization conditions, wherein polymorphic loci corresponding to the SNP-ASOs are present with a frequency of at least 50% in a RCG made using the at least one PCR primer and

determining the presence or absence of a SNP allele in the RCG by hybridization of the RCG with a SNP-ASO to identify a genotype.

150. (Previously presented) The method of claim 149, wherein the RCG contains less than 5% of genomic material present in a whole genome.

151. (Previously presented) The method of claim 149, wherein the RCG contains less than 1% of genomic material present in a whole genome.

152. (Previously presented) The method of claim 149, wherein the RCG contains less than 0.05% of genomic material present in a whole genome.

153. (Currently amended) The method of any one of claims 149-150, wherein the at least one PCR primer is a primer for degenerate oligonucleotide priming-PCR (DOP-PCR).

154. (Previously presented) The method of any one of claims 149-150, wherein the at least one PCR primer is a primer for adapter-PCR.
155. (Previously presented) The method of claim 149, wherein the SNP-ASOs are composed of between 10 and 50 nucleotide residues.
156. (Previously presented) The method of claim 149, wherein the SNP-ASOs are composed of between 10 and 25 nucleotide residues.
157. (Currently amended) A method comprising:
preparing a randomly primed PCR-derived reduced complexity genome (RCG) from a genome of a tumor cell using at least one polymerase chain reaction (PCR) primer, wherein the RCG contains less than 20% of genomic material present in a whole genome,
contacting single nucleotide polymorphisms – allele specific oligonucleotides (SNP-ASOs) immobilized on a surface with the RCG under hybridization conditions, wherein polymorphic loci associated with SNPs corresponding to the SNP-ASOs are present with a frequency of at least 50% in a RCG made using the at least one PCR primer, and
determining the presence or absence of a SNP allele in the RCG by hybridization of the RCG with a SNP-ASO to identify a loss of heterozygosity in the tumor.
158. (Previously presented) The method of claim 157, wherein the RCG contains less than 5% of genomic material present in a whole genome.
159. (Currently amended) The method of any one of claims 157-158, wherein the at least one PCR primer is a primer for degenerate oligonucleotide priming-PCR (DOP-PCR).
160. (Previously presented) The method of any one of claims 157-158, wherein the at least one PCR primer is a primer for adapter-PCR.

161-164. (Canceled).

165. (Previously presented) A method for simultaneously detecting a plurality of single nucleotide polymorphism (SNP) alleles in a genomic DNA sample which comprises:

preparing a randomly-primed PCR-derived reduced complexity genome (RCG) from the genomic DNA sample;

hybridizing said RCG with an arrayed panel of oligonucleotides indicative of SNP alleles associated with said RCG; and

analyzing the hybridization pattern of said RCG with oligonucleotides to thereby determine the presence or absence of said SNP alleles.

166. (Previously presented) A method for genotyping single nucleotide polymorphism (SNP) alleles in a genomic DNA sample of a subject which comprises:

preparing a randomly-primed PCR-derived reduced complexity genome (RCG) from the genomic DNA sample;

hybridizing said RCG with an arrayed panel of SNP alleles specific for said RCG; and

analyzing the hybridization pattern of said RCG on said panel to thereby determine a genotype of said subject.